K. Davis

1600

ENTERED #18
3-25-02
KFD

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,274B

DATE: 03/19/2002
TIME: 14:10:29

Input Set : **A:\00100301.app**
Output Set: **N:\CRF3\03192002\I435274B.raw**

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 3 <110> APPLICANT: Citovsky, Vitaly H
 4       Rhee, Yoon
 6 <120> TITLE OF INVENTION: Genetic Assay for Protein Nuclear Transport
 8 <130> FILE REFERENCE: 001.00301
10 <140> CURRENT APPLICATION NUMBER: US 09/435,274B
11 <141> CURRENT FILING DATE: 1999-11-05
13 <150> PRIOR APPLICATION NUMBER: US 60/107,417
14 <151> PRIOR FILING DATE: 1998-11-06
16 <160> NUMBER OF SEQ ID NOS: 17
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 611
22 <212> TYPE: DNA
23 <213> ORGANISM: Unknown Organism
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
28 <220> FEATURE:
29 <223> OTHER INFORMATION: modified bacterial lexA
31 <400> SEQUENCE: 1
32 atgaaagcgt taacggccag gcaacaagag gtgtttgatc tcatccgtga tcacatcagc 60
33 cagacaggta tgccgccgac gcgtgcggaa atcgcgcagc gtttgggggtt cgttccccaa 120
34 acgcggctga agaacatctg aaggcgctgg cacgcaaagg cgttattgaa attgtttccg 180
35 gcgcatcacg cgggattcgt ctgttgcagg aagaggaaga agggttgccg ctggtaggtc 240
36 gtgtggctgc cggtgaacca cttctggcgc aacagcatat tgaaggtcat tatcaggtcg 300
37 atccttcctt attcaagccg aatgctgatt tcctgctgcg cgtcagcggg atgtcgatga 360
38 aagatatcgg cattatggat ggtgacttgc tggcagtgca taaaactcag gatgtacgta 420
39 acggtcaggt cgttgtcgca cgtattgatg acgaagttac cgttaagggc ctggaaaaac 480
40 agggcaataa agtcgaactg ttgccagaaa atagcgagtt taaaccaatt gtcgttgacc 540
41 ttcgtcagca gagcttcacc attgaagggc tggcggttgg ggttattcgc aacggcgact 600
42 ggctggaatt c                                                  611
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 204
47 <212> TYPE: PRT
48 <213> ORGANISM: Unknown Organism
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
53 <220> FEATURE:
54 <223> OTHER INFORMATION: modified bacterial lexA
56 <400> SEQUENCE: 2
57 Met Lys Ala Leu Thr Ala Arg Gln Gln Glu Val Phe Asp Leu Ile Arg
58  1               5                   10                  15
60 Asp His Ile Ser Gln Thr Gly Met Pro Pro Thr Arg Ala Glu Ile Ala
61              20                  25                  30
```

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63 Gln Arg Leu Gly Phe Arg Ser Pro Asn Ala Ala Glu Glu His Leu Lys
64          35              40              45
66 Ala Leu Ala Arg Lys Gly Val Ile Glu Ile Val Ser Gly Ala Ser Arg
67       50              55              60
69 Gly Ile Arg Leu Leu Gln Glu Glu Glu Glu Gly Leu Pro Leu Val Gly
70  65              70              75              80
72 Arg Val Ala Ala Gly Glu Pro Leu Leu Ala Gln Gln His Ile Glu Gly
73              85              90              95
75 His Tyr Gln Val Asp Pro Ser Leu Phe Lys Pro Asn Ala Asp Phe Leu
76          100             105             110
78 Leu Arg Val Ser Gly Met Ser Met Lys Asp Ile Gly Ile Met Asp Gly
79          115             120             125
81 Asp Leu Leu Ala Val His Lys Thr Gln Asp Val Arg Asn Gly Gln Val
82      130             135             140
84 Val Val Ala Arg Ile Asp Asp Glu Val Thr Val Lys Gly Leu Glu Lys
85 145             150             155             160
87 Gln Gly Asn Lys Val Glu Leu Leu Pro Glu Asn Ser Glu Phe Lys Pro
88              165             170             175
90 Ile Val Val Asp Leu Arg Gln Gln Ser Phe Thr Ile Glu Gly Leu Ala
91          180             185             190
93 Val Gly Val Ile Arg Asn Gly Asp Trp Leu Glu Phe
94          195             200
```

97 <210> SEQ ID NO: 3
98 <211> LENGTH: 7
99 <212> TYPE: PRT
100 <213> ORGANISM: Simian virus 40
102 <220> FEATURE:
103 <223> OTHER INFORMATION: large T antigen NLS
105 <400> SEQUENCE: 3
106 Pro Lys Lys Lys Arg Lys Val
107   1   5
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 17
112 <212> TYPE: PRT
113 <213> ORGANISM: Xenopus sp.
115 <220> FEATURE:
116 <223> OTHER INFORMATION: nucleoplasmin NLS
118 <220> FEATURE:
119 <221> NAME/KEY: VARIANT
120 <222> LOCATION: (3)..(13)
121 <223> OTHER INFORMATION: Residues 3 to 13 in Xenopus laevis are Pro Ala Ala
122   Thr Lys Lys Ala Gly Gln Ala Lys
124 <400> SEQUENCE: 4
W--> 125 Lys Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Lys Lys
126   1   5   10   15
128 Leu
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 9
134 <212> TYPE: PRT

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135 <213> ORGANISM: Human immunodeficiency virus type 1
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Rev protein NES
140 <400> SEQUENCE: 5
141 Leu Pro Pro Leu Glu Arg Leu Thr Leu
142    1               5
145 <210> SEQ ID NO: 6
146 <211> LENGTH: 9
147 <212> TYPE: PRT
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
152       signal
154 <220> FEATURE:
155 <223> OTHER INFORMATION: mutated NES of pNEAM10
157 <400> SEQUENCE: 6
158 Leu Pro Pro Asp Leu Arg Leu Thr Leu
159    1               5
162 <210> SEQ ID NO: 7
163 <211> LENGTH: 4
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
169       signal
171 <220> FEATURE:
172 <223> OTHER INFORMATION: residual NES of pNEARev(delta)3
174 <400> SEQUENCE: 7
175 Leu Pro Pro Leu
176    1
179 <210> SEQ ID NO: 8
180 <211> LENGTH: 26
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: GAL4 primer
190 <400> SEQUENCE: 8
191 gggaattcaa ttttaatcaa agtggg                              26
194 <210> SEQ ID NO: 9
195 <211> LENGTH: 27
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: GAL4 primer
205 <400> SEQUENCE: 9
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206 gacggatccc cgggtattcg atctctt                                    27
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210 <211> LENGTH: 29
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: GAL4 primer
220 <400> SEQUENCE: 10
221 gggaattcga taaagcggaa ttaattccc                                   29
224 <210> SEQ ID NO: 11
225 <211> LENGTH: 27
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: GAL4 primer
235 <400> SEQUENCE: 11
236 gacggatccc cgggtattcg atctctt                                    27
239 <210> SEQ ID NO: 12
240 <211> LENGTH: 25
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: mutant lexA primer
250 <400> SEQUENCE: 12
251 ccgttaaggg cctggaaaaa caggg                                      25
254 <210> SEQ ID NO: 13
255 <211> LENGTH: 26
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: selection lexA primer
265 <400> SEQUENCE: 13
266 gtgactggtg aggcctcaac caagtc                                     26
269 <210> SEQ ID NO: 14
270 <211> LENGTH: 33
271 <212> TYPE: DNA
272 <213> ORGANISM: Escherichia coli
274 <400> SEQUENCE: 14
275 gttaccgtta agcgcctgaa aaacagggc aat                              33
278 <210> SEQ ID NO: 15
279 <211> LENGTH: 11
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```
280 <212> TYPE: PRT
281 <213> ORGANISM: Escherichia coli
283 <400> SEQUENCE: 15
284 Val Thr Val Lys Arg Leu Lys Lys Gln Gly Asn
285   1               5                   10
288 <210> SEQ ID NO: 16
289 <211> LENGTH: 11
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence:MODIFIED
295       BACTERIAL LEX A
297 <400> SEQUENCE: 16
298 Val Thr Val Lys Gly Leu Glu Lys Gln Gly Asn
299   1               5                   10
302 <210> SEQ ID NO: 17
303 <211> LENGTH: 33
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:MODIFIED
309       BACTERIAL LEX A
311 <400> SEQUENCE: 17
312 gttaccgtta agggcctgga aaaacagggc aat                          33
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VERIFICATION SUMMARY   DATE: 03/19/2002
PATENT APPLICATION: **US/09/435,274B**   TIME: 14:10:30

Input Set : **A:\00100301.app**
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L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4